

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/538,704  
Source: PCR  
Date Processed by STIC: 3/16/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 03/16/2006

PATENT APPLICATION: US/10/538,704

TIME: 12:39:31

Input Set : N:\Crf4\03142006\J538704.raw

Output Set: N:\CRF4\03162006\J538704.raw

```

1 <110> APPLICANT: Olayioye, Monilola
2   Visvader, Jane
3   Lindeman, Geoffrey
4   Hoffmann, Peter
5   Pomorski, Thomas
6 <120> TITLE OF INVENTION: A NOVEL PHOSPHOPROTEIN
7 <130> FILE REFERENCE: DAVI186.004APC
8 <140> CURRENT APPLICATION NUMBER: US/10/538,704
9 <141> CURRENT FILING DATE: 2005-06-10
10 <150> PRIOR APPLICATION NUMBER: PCT/AU03/01664
11 <151> PRIOR FILING DATE: 2003-12-12
12 <150> PRIOR APPLICATION NUMBER: AU 2002953341
13 <151> PRIOR FILING DATE: 2002-12-13
14 <160> NUMBER OF SEQ ID NOS: 7
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 13
19 <212> TYPE: PRT
20 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: peptide
23 <400> SEQUENCE: 1
24   Glu Ser Ala Val Ala Glu Ser Arg Glu Glu Arg Met Gly
25       1             5             10
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 18
29 <212> TYPE: PRT
30 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: peptide
33 <400> SEQUENCE: 2
34   Gln His Ala Asp Ser Leu Glu Asn Ile Asp Glu Ser Ala Val Ala Glu
35       1             5             10             15
36   Ser Arg
38 <210> SEQ ID NO: 3
39 <211> LENGTH: 18
40 <212> TYPE: PRT
41 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: peptide
44 <400> SEQUENCE: 3
45   Arg Arg Ala Ala Ser Met Asp Asn Asn Ser Lys Phe Ala Lys Ser Arg
46       1             5             10             15

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47      Ser Arg
49 <210> SEQ ID NO: 4
50 <211> LENGTH: 876
51 <212> TYPE: DNA
52 <213> ORGANISM: Homo sapiens
53 <400> SEQUENCE: 4
54      atggagaagc tggcggcctc tacagagccc caagggcctc ggccggtcct gggccgtgag 60
55      agtgtccagg tgcccgatga ccaagacttt cgcagcttcc ggtcagagtg tgaggctgag 120
56      gtgggctgga acctgacctg tagcagggtc ggggtgtctg tctgggtgca ggctgtggag 180
57      atggatcgga cgctgcacaa gatcaagtgc cggatggagt gctgtgatgt gccagccgag 240
58      acactctacg acgtcctaca cgacattgag taccgcaaga aatgggacag caacgtcatt 300
59      gagacttttg acatcgcccg cttgacagtc aacgctgacg tgggctatta ctctggagg 360
60      tgtcccaagc ccctgaagaa ccgtgatgtc atcaccctcc gctcctggct ccccatgggc 420
61      gctgattaca tcattatgaa ctactcagtc aaacatccca aatacccacc tcggaagagc 480
62      ttgggtccgag ctgtgtccat ccagacgggc tacctcatcc agagcacagg gcccaagagc 540
63      tgcgtcatca cctacctggc ccaggtggac cccaaaggct ccttacccaa gtgggtgggtg 600
64      aataaatctt ctcagttcct ggctcccaag gccatgaaga agatgtacaa ggctgcctc 660
65      aagtaccccg agtggaaaca gaagcacctg cctcacttca agccgtgggt gcacccggag 720
66      cagagcccg tgcgagcct ggcgctgtcg gagctgtcgg tgcagcatgc ggactcactg 780
67      gagaacatcg acgagagcgc ggtggccgag agcagagagg agcggatggg cggcgcgggc 840
68      ggcgagggca gcgacgacga cacctcgctc acctga 876
70 <210> SEQ ID NO: 5
71 <211> LENGTH: 291
72 <212> TYPE: PRT
73 <213> ORGANISM: Homo sapiens
74 <400> SEQUENCE: 5
75      Met Glu Lys Leu Ala Ala Ser Thr Glu Pro Gln Gly Pro Arg Pro Val
76      1          5          10          15
77      Leu Gly Arg Glu Ser Val Gln Val Pro Asp Asp Gln Asp Phe Arg Ser
78      20          25          30
79      Phe Arg Ser Glu Cys Glu Ala Glu Val Gly Trp Asn Leu Thr Tyr Ser
80      35          40          45
81      Arg Ala Gly Val Ser Val Trp Val Gln Ala Val Glu Met Asp Arg Thr
82      50          55          60
83      Leu His Lys Ile Lys Cys Arg Met Glu Cys Cys Asp Val Pro Ala Glu
84      65          70          75          80
85      Thr Leu Tyr Asp Val Leu His Asp Ile Glu Tyr Arg Lys Lys Trp Asp
86      85          90          95
87      Ser Asn Val Ile Glu Thr Phe Asp Ile Ala Arg Leu Thr Val Asn Ala
88      100         105         110
89      Asp Val Gly Tyr Tyr Ser Trp Arg Cys Pro Lys Pro Leu Lys Asn Arg
90      115         120         125
91      Asp Val Ile Thr Leu Arg Ser Trp Leu Pro Met Gly Ala Asp Tyr Ile
92      130         135         140
93      Ile Met Asn Tyr Ser Val Lys His Pro Lys Tyr Pro Pro Arg Lys Asp
94      145         150         155         160
95      Leu Val Arg Ala Val Ser Ile Gln Thr Gly Tyr Leu Ile Gln Ser Thr
96      165         170         175
97      Gly Pro Lys Ser Cys Val Ile Thr Tyr Leu Ala Gln Val Asp Pro Lys

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98          180          185          190
99      Gly Ser Leu Pro Lys Trp Val Val Asn Lys Ser Ser Gln Phe Leu Ala
100          195          200          205
101      Pro Lys Ala Met Lys Lys Met Tyr Lys Ala Cys Leu Lys Tyr Pro Glu
102          210          215          220
103      Trp Lys Gln Lys His Leu Pro His Phe Lys Pro Trp Leu His Pro Glu
104          225          230          235          240
105      Gln Ser Pro Leu Pro Ser Leu Ala Leu Ser Glu Leu Ser Val Gln His
106          245          250          255
107      Ala Asp Ser Leu Glu Asn Ile Asp Glu Ser Ala Val Ala Glu Ser Arg
108          260          265          270
109      Glu Glu Arg Met Gly Gly Ala Gly Gly Glu Gly Ser Asp Asp Asp Thr
110          275          280          285
111      Ser Leu Thr
112          290
114 <210> SEQ ID NO: 6
115 <211> LENGTH: 359
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
118 <400> SEQUENCE: 6
119      Met Ser Thr Arg Ala Lys Lys Leu Arg Arg Ile Trp Arg Ile Leu Glu
120          1          5          10          15
121      Glu Glu Glu Ser Val Ala Gly Ala Val Gln Thr Leu Leu Leu Arg Ser
122          20          25          30
123      Gln Glu Gly Gly Val Thr Ser Ala Ala Ala Ser Thr Leu Ser Glu Pro
124          35          40          45
125      Pro Arg Arg Thr Gln Glu Ser Arg Thr Arg Thr Arg Ala Leu Gly Leu
126          50          55          60
127      Pro Thr Leu Pro Met Glu Lys Leu Ala Ala Ser Thr Glu Pro Gln Gly
128          65          70          75          80
129      Pro Arg Pro Val Leu Gly Arg Glu Ser Val Gln Val Pro Asp Asp Gln
130          85          90          95
131      Asp Phe Arg Ser Phe Arg Ser Glu Cys Glu Ala Glu Val Gly Trp Asn
132          100          105          110
133      Leu Thr Tyr Ser Arg Ala Gly Val Ser Val Trp Val Gln Ala Val Glu
134          115          120          125
135      Met Asp Arg Thr Leu His Lys Ile Lys Cys Arg Met Glu Cys Cys Asp
136          130          135          140
137      Val Pro Ala Glu Thr Leu Tyr Asp Val Leu His Asp Ile Glu Tyr Arg
138          145          150          155          160
139      Lys Lys Trp Asp Ser Asn Val Ile Glu Thr Phe Asp Ile Ala Arg Leu
140          165          170          175
141      Thr Val Asn Ala Asp Val Gly Tyr Tyr Ser Trp Arg Cys Pro Lys Pro
142          180          185          190
143      Leu Lys Asn Arg Asp Val Ile Thr Leu Arg Ser Trp Leu Pro Met Gly
144          195          200          205
145      Ala Asp Tyr Ile Ile Met Asn Tyr Ser Val Lys His Pro Lys Tyr Pro
146          210          215          220
147      Pro Arg Lys Asp Leu Val Arg Ala Val Ser Ile Gln Thr Gly Tyr Leu

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148      225      230      235      240
149      Ile Gln Ser Thr Gly Pro Lys Ser Cys Val Ile Thr Tyr Leu Ala Gln
150      245      250      255
151      Val Asp Pro Lys Gly Ser Leu Pro Lys Trp Val Val Asn Lys Ser Ser
152      260      265      270
153      Gln Phe Leu Ala Pro Lys Ala Met Lys Lys Met Tyr Lys Ala Cys Leu
154      275      280      285
155      Lys Tyr Pro Glu Trp Lys Gln Lys His Leu Pro His Phe Lys Pro Trp
156      290      295      300
157      Leu His Pro Glu Gln Ser Pro Leu Pro Ser Leu Ala Leu Ser Glu Leu
158      305      310      315      320
159      Ser Val Gln His Ala Asp Ser Leu Glu Asn Ile Asp Glu Ser Ala Val
160      325      330      335
161      Ala Glu Ser Arg Glu Glu Arg Met Gly Gly Ala Gly Gly Glu Gly Ser
162      340      345      350
163      Asp Asp Asp Thr Ser Leu Thr
164      355
166 <210> SEQ ID NO: 7
167 <211> LENGTH: 214
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
170 <400> SEQUENCE: 7
171      Met Glu Leu Ala Ala Gly Ser Phe Ser Glu Glu Gln Phe Trp Glu Ala
172      1      5      10      15
173      Cys Ala Glu Leu Gln Gln Pro Ala Leu Ala Gly Ala Asp Trp Gln Leu
174      20      25      30
175      Leu Val Glu Thr Ser Gly Ile Ser Ile Tyr Arg Leu Leu Asp Lys Lys
176      35      40      45
177      Thr Gly Leu His Glu Tyr Lys Val Phe Gly Val Leu Glu Asp Cys Ser
178      50      55      60
179      Pro Thr Leu Leu Ala Asp Ile Tyr Met Asp Ser Asp Tyr Arg Lys Gln
180      65      70      75      80
181      Trp Asp Gln Tyr Val Lys Glu Leu Tyr Glu Gln Glu Cys Asn Gly Glu
182      85      90      95
183      Thr Val Val Tyr Trp Glu Val Lys Tyr Pro Phe Pro Met Ser Asn Arg
184      100      105      110
185      Asp Tyr Val Tyr Leu Arg Gln Arg Asp Leu Asp Met Glu Gly Arg
186      115      120      125
187      Lys Ile His Val Ile Leu Ala Arg Ser Thr Ser Met Pro Gln Leu Gly
188      130      135      140
189      Glu Arg Ser Gly Val Ile Arg Val Lys Gln Tyr Lys Gln Ser Leu Ala
190      145      150      155      160
191      Ile Glu Ser Asp Gly Lys Lys Gly Ser Lys Val Phe Met Tyr Tyr Phe
192      165      170      175
193      Asp Asn Pro Gly Gly Gln Ile Pro Ser Trp Leu Ile Asn Trp Ala Ala
194      180      185      190
195      Lys Asn Gly Val Pro Asn Phe Leu Lys Asp Met Ala Arg Ala Cys Gln
196      195      200      205
197      Asn Tyr Leu Lys Lys Thr

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**VERIFICATION SUMMARY**

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